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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2011; month=1; day=31; hr=15; min=51; sec=38; ms=517;]

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Reviewer Comments:

<210> 9

<211> 1743

<212> PRT

<213> Escherichia coli

<400> 9

(errored portion shown below)

Gly Ser Val Ala Asn Glu Glu Asn Thr Ile Ser Val Gly Ser Ser

1550

1555

1560

Please remove the blank line between the above amino acid numbers and their respective amino acids. Amino acid numbers must appear directly below their amino acids. Please ensure that the amino acid numbers are properly aligned (do not use TAB codes between amino acid numbers: TABs cause misalignment).

<210> 10

<211> 4684

<212> PRT

<213> Escherichia coli

<400> 10

(errored portions shown below)

Ala Asp Gly Lys Thr Ala Gly Asn Thr Ala Lys Ala Tyr Met Ser

1595

1600

1605

Please remove the blank line between the above amino acid numbers and their respective amino acids.

(also in Sequence 10)

Asn Leu Thr Ala Gly Ser Thr Asp Ala Val Asn Gly Ser Gln Leu

3515

3520

3525

Please remove the blank line between the above amino acid numbers and their amino acids.

<210> 16

<211> 372

<212> PRT

<213> Bradorhizobium japonicum

<400> 16

(errored portion shown below)

Ala Leu Ala Ala Ser Ser Leu Gln Phe Asp Pro Arg Pro Gly Lys Ile

305

310

315

320

Please remove the blank line between the above amino acid numbers and their respective amino acids.

Application No: 10562191

Version No: 3.0

Input Set:**Output Set:**

Started: 2011-01-21 15:33:41.884
Finished: 2011-01-21 15:33:50.393
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 509 ms
Total Warnings: 44
Total Errors: 8
No. of SeqIDs Defined: 107
Actual SeqID Count: 107

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (4)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (10)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (10)
W 402	Undefined organism found in <213> in SEQ ID (16)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (31)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)

Input Set:

Output Set:

Started: 2011-01-21 15:33:41.884
Finished: 2011-01-21 15:33:50.393
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 509 ms
Total Warnings: 44
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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (44)
W 213	Artificial or Unknown found in <213> in SEQ ID (45)
W 213	Artificial or Unknown found in <213> in SEQ ID (46)
W 213	Artificial or Unknown found in <213> in SEQ ID (47)
W 213	Artificial or Unknown found in <213> in SEQ ID (48)
W 213	Artificial or Unknown found in <213> in SEQ ID (49)
W 402	Undefined organism found in <213> in SEQ ID (50)
W 402	Undefined organism found in <213> in SEQ ID (51)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
W 402	Undefined organism found in <213> in SEQ ID (53)
W 402	Undefined organism found in <213> in SEQ ID (54)
W 402	Undefined organism found in <213> in SEQ ID (56)
W 402	Undefined organism found in <213> in SEQ ID (57)
W 402	Undefined organism found in <213> in SEQ ID (58)
W 402	Undefined organism found in <213> in SEQ ID (59)
W 402	Undefined organism found in <213> in SEQ ID (60)
W 402	Undefined organism found in <213> in SEQ ID (61)
W 402	Undefined organism found in <213> in SEQ ID (65)
W 402	Undefined organism found in <213> in SEQ ID (72)
W 402	Undefined organism found in <213> in SEQ ID (78)
W 402	Undefined organism found in <213> in SEQ ID (92)
	This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (106)

SEQUENCE LISTING

<110> MASIGNANI, Vega
ARICO, Maria Beatrice

<120> VIRULENCE-ASSOCIATED ADHESINS

<130> 2300-20667

<140> 10562191

<141> 2011-01-21

<150> PCT/IB2004/002351

<151> 2004-06-25

<150> GB 0315022.4

<151> 2003-06-26

<160> 107

<170> PatentIn version 3.5

<210> 1

<211> 223

<212> PRT

<213> Haemophilus aegyptius

<400> 1

Met	Lys	Arg	Asn	Leu	Leu	Lys	Gln	Ser	Val	Ile	Ala	Val	Leu	Ile	Gly
1				5					10					15	

Gly	Thr	Thr	Val	Ser	Asn	Tyr	Ala	Leu	Ala	Gln	Ala	Gln	Ala	Gln	Ala
			20					25					30		

Gln	Val	Lys	Lys	Asp	Glu	Leu	Ser	Glu	Leu	Lys	Lys	Gln	Val	Lys	Glu
		35					40					45			

Met	Asp	Ala	Ala	Ile	Asp	Gly	Ile	Leu	Asp	Asp	Asn	Ile	Ala	Tyr	Glu
	50					55					60				

Ala	Glu	Val	Asp	Ala	Lys	Leu	Asp	Gln	His	Ser	Ala	Ala	Leu	Gly	Arg
65					70				75					80	

His	Thr	Asn	Arg	Leu	Asn	Asn	Leu	Lys	Thr	Ile	Ala	Glu	Lys	Ala	Lys
				85					90					95	

Gly	Asp	Ser	Ser	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Ala	Leu	Glu	Glu	Gln
				100				105					110		

Asn Asp Glu Phe Leu Ala Asp Ile Thr Ala Leu Glu Glu Gly Val Asp
 115 120 125

Gly Leu Asp Asp Asp Ile Ala Gly Ile Gln Asp Asn Ile Ser Asp Ile
 130 135 140

Glu Asp Asp Ile Asn Gln Asn Ser Ala Asp Ile Ala Thr Asn Thr Ala
 145 150 155 160

Ala Ile Ala Thr His Thr Gln Arg Leu Asp Asn Leu Asp Asn Arg Val
 165 170 175

Asn Asn Leu Asn Lys Asp Leu Lys Arg Gly Leu Ala Ala Gln Ala Ala
 180 185 190

Leu Asn Gly Leu Phe Gln Pro Tyr Asn Val Gly Lys Leu Asn Leu Thr
 195 200 205

Ala Ala Val Gly Gly Tyr Lys Ser Gln Thr Ala Val Ala Val Gly
 210 215 220

<210> 2
 <211> 338
 <212> PRT
 <213> Escherichia coli

<400> 2

Met Lys Thr Val Asn Val Ala Leu Leu Ala Leu Ile Ile Ser Ala Thr
 1 5 10 15

Ser Ser Pro Val Val Leu Ala Gly Asp Thr Ile Glu Ala Ala Ala Thr
 20 25 30

Glu Leu Ser Ala Ile Asn Ser Gly Met Ser Gln Ser Glu Ile Glu Gln
 35 40 45

Lys Ile Thr Arg Phe Leu Glu Arg Thr Asp Asn Ser Pro Ala Ala Tyr
 50 55 60

Thr Tyr Leu Thr Glu His His Tyr Ile Pro Ser Glu Thr Pro Asp Thr
 65 70 75 80

Thr Gln Thr Pro Thr Val Gln Thr Asp Pro Asp Ala Gly Gln Lys Thr
85 90 95

Val Ala Ala Thr Gly Asp Val Gln Thr Thr Ala Arg Tyr Gln Ser Met
100 105 110

Ile Asn Ala Arg Gln Ser Ala Val Thr Asp Ala Gln Gln Thr Gln Ile
115 120 125

Thr Glu Gln Gln Ala Gln Ile Val Ala Thr Gln Lys Thr Leu Ala Ala
130 135 140

Thr Gly Asp Thr Gln Asn Thr Ala His Tyr Gln Glu Met Ile Asn Ala
145 150 155 160

Arg Leu Ala Ala Gln Asn Glu Ala Asn Gln Arg Thr Ala Thr Glu Gln
165 170 175

Gly Gln Lys Met Asn Ala Leu Thr Thr Asp Val Ala Val Gln Gln Gln
180 185 190

Asn Glu Arg Thr Gln Tyr Asp Lys Gln Met Gln Ser Leu Ala Gln Glu
195 200 205

Ser Ala Gln Ala His Glu Gln Ile Asp Ser Leu Ser Gln Asp Val Thr
210 215 220

Gln Thr His Gln Gln Leu Thr Asn Thr Gln Lys Arg Val Ala Asp Asn
225 230 235 240

Ser Gln Gln Ile Asn Thr Leu Asn Asn His Phe Ser Ser Leu Lys Asn
245 250 255

Glu Val Asp Asp Asn Arg Lys Glu Ala Asn Ala Gly Thr Ala Ser Ala
260 265 270

Ile Ala Ile Ala Ser Gln Pro Gln Val Lys Thr Gly Asp Val Met Met
275 280 285

Val Ser Ala Gly Ala Gly Thr Phe Asn Gly Glu Ser Ala Val Ser Val
290 295 300

Gly Thr Ser Phe Asn Ala Gly Thr His Thr Val Leu Lys Ala Gly Ile

305 310 315 320

Ser Ala Asp Thr Gln Ser Asp Phe Gly Ala Gly Val Gly Val Gly Tyr
325 330 335

Ser Phe

<210> 3
<211> 1588
<212> PRT
<213> Escherichia coli

<400> 3

Met Asn Lys Ile Phe Lys Val Ile Trp Asn Pro Ala Thr Gly Asn Tyr
1 5 10 15

Thr Val Thr Ser Glu Thr Ala Lys Ser Arg Gly Lys Lys Ser Gly Arg
20 25 30

Ser Lys Leu Leu Ile Ser Ala Leu Val Ala Gly Gly Met Leu Ser Ser
35 40 45

Phe Gly Ala Leu Ala Asn Ala Gly Asn Asp Asn Gly Gln Gly Val Asp
50 55 60

Tyr Gly Ser Gly Ser Ala Gly Asp Gly Trp Val Ala Ile Gly Lys Gly
65 70 75 80

Ala Lys Ala Asn Thr Phe Met Asn Thr Ser Gly Ser Ser Thr Ala Val
85 90 95

Gly Tyr Asp Ala Ile Ala Glu Gly Gln Tyr Ser Ser Ala Ile Gly Ser
100 105 110

Lys Thr His Ala Ile Gly Gly Ala Ser Met Ala Phe Gly Val Ser Ala
115 120 125

Ile Ser Glu Gly Asp Arg Ser Ile Ala Leu Gly Ala Ser Ser Tyr Ser
130 135 140

Leu Gly Gln Tyr Ser Met Ala Leu Gly Arg Tyr Ser Lys Ala Leu Gly
145 150 155 160

Lys Leu Ser Ile Ala Met Gly Asp Ser Ser Lys Ala Glu Gly Ala Asn
 165 170 175

Ala Ile Ala Leu Gly Asn Ala Thr Lys Ala Thr Glu Ile Met Ser Ile
 180 185 190

Ala Leu Gly Asp Thr Ala Asn Ala Ser Lys Ala Tyr Ser Met Ala Leu
 195 200 205

Gly Ala Ser Ser Val Ala Ser Glu Glu Asn Ala Ile Ala Ile Gly Ala
 210 215 220

Glu Thr Glu Ala Ala Glu Asn Ala Thr Ala Ile Gly Asn Asn Ala Lys
 225 230 235 240

Ala Lys Gly Thr Asn Ser Met Ala Met Gly Phe Gly Ser Leu Ala Asp
 245 250 255

Lys Val Asn Thr Ile Ala Leu Gly Asn Gly Ser Gln Ala Leu Ala Asp
 260 265 270

Asn Ala Ile Ala Ile Gly Gln Gly Asn Lys Ala Asp Gly Val Asp Ala
 275 280 285

Ile Ala Leu Gly Asn Gly Ser Gln Ser Arg Gly Leu Asn Thr Ile Ala
 290 295 300

Leu Gly Thr Ala Ser Asn Ala Thr Gly Asp Lys Ser Leu Ala Leu Gly
 305 310 315 320

Ser Asn Ser Ser Ala Asn Gly Ile Asn Ser Val Ala Leu Gly Ala Asp
 325 330 335

Ser Ile Ala Asp Leu Asp Asn Thr Val Ser Val Gly Asn Ser Ser Leu
 340 345 350

Lys Arg Lys Ile Val Asn Val Lys Asn Gly Ala Ile Lys Ser Asp Ser
 355 360 365

Tyr Asp Ala Ile Asn Gly Ser Gln Leu Tyr Ala Ile Ser Asp Ser Val
 370 375 380

Ala Lys Arg Leu Gly Gly Gly Ala Ala Val Asp Val Asp Asp Gly Thr
385 390 395 400

Val Thr Ala Pro Thr Tyr Asn Leu Lys Asn Gly Ser Lys Asn Asn Val
405 410 415

Gly Ala Ala Leu Ala Val Leu Asp Glu Asn Thr Leu Gln Trp Asp Gln
420 425 430

Thr Lys Gly Lys Tyr Ser Ala Ala His Gly Thr Ser Ser Pro Thr Ala
435 440 445

Ser Val Ile Thr Asp Val Ala Asp Gly Thr Ile Ser Ala Ser Ser Lys
450 455 460

Asp Ala Val Asn Gly Ser Gln Leu Lys Ala Thr Asn Asp Asp Val Glu
465 470 475 480

Ala Asn Thr Ala Asn Ile Ala Thr Asn Thr Ser Asn Ile Ala Thr Asn
485 490 495

Thr Ala Asn Ile Ala Thr Asn Thr Thr Asn Ile Thr Asn Leu Thr Asp
500 505 510

Ser Val Gly Asp Leu Gln Ala Asp Ala Leu Leu Trp Asn Glu Thr Lys
515 520 525

Lys Ala Phe Ser Ala Ala His Gly Gln Asp Thr Thr Ser Lys Ile Thr
530 535 540

Asn Val Lys Asp Ala Asp Leu Thr Ala Asp Ser Thr Asp Ala Val Asn
545 550 555 560

Gly Ser Gln Leu Lys Thr Thr Asn Asp Ala Val Ala Thr Asn Thr Thr
565 570 575

Asn Ile Ala Asn Asn Thr Ser Asn Ile Ala Thr Asn Thr Thr Asn Ile
580 585 590

Ser Asn Leu Thr Glu Thr Val Thr Asn Leu Gly Glu Asp Ala Leu Lys
595 600 605

Trp Asp Lys Asp Asn Gly Val Phe Thr Ala Ala His Gly Thr Glu Thr

610		615		620	
Thr Ser Lys Ile Thr	Asn Val Lys Asp Gly Asp Leu Thr Thr Gly Ser				
625	630	635	640		
Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Ala Val					
	645	650	655		
Ala Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn Ile Ser Asn					
	660	665	670		
Leu Thr Glu Thr Val Thr Asn Leu Gly Glu Asp Ala Leu Lys Trp Asp					
	675	680	685		
Lys Asp Asn Gly Val Phe Thr Ala Ala His Gly Asn Asn Thr Ala Ser					
	690	695	700		
Lys Ile Thr Asn Ile Leu Asp Gly Thr Val Thr Ala Thr Ser Ser Asp					
705	710	715	720		
Ala Ile Asn Gly Ser Gln Leu Tyr Asp Leu Ser Ser Asn Ile Ala Thr					
	725	730	735		
Tyr Phe Gly Gly Asn Ala Ser Val Asn Thr Asp Gly Val Phe Thr Gly					
	740	745	750		
Pro Thr Tyr Lys Ile Gly Glu Thr Asn Tyr Tyr Asn Val Gly Asp Ala					
	755	760	765		
Leu Ala Ala Ile Asn Ser Ser Phe Ser Thr Ser Leu Gly Asp Ala Leu					
	770	775	780		
Leu Trp Asp Ala Thr Ala Gly Lys Phe Ser Ala Lys His Gly Thr Asn					
785	790	795	800		
Gly Asp Ala Ser Val Ile Thr Asp Val Ala Asp Gly Glu Ile Ser Asp					
	805	810	815		
Ser Ser Ser Asp Ala Val Asn Gly Ser Gln Leu His Gly Val Ser Ser					
	820	825	830		
Tyr Val Val Asp Ala Leu Gly Gly Gly Ala Glu Val Asn Ala Asp Gly					
	835	840	845		

Thr Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Asp Tyr Asp Asn
850 855 860

Val Gly Asp Ala Leu Asn Ala Ile Asp Thr Thr Leu Asp Asp Ala Leu
865 870 875 880

Leu Trp Asp Ala Asp Ala Gly Glu Asn Gly Ala Phe Ser Ala Ala His
885 890 895

Gly Lys Asp Lys Thr Ala Ser Val Ile Thr Asn Val Ala Asn Gly Ala
900 905 910

Ile Ser Ala Ala Ser Ser Asp Ala Ile Asn Gly Ser Gln Leu Tyr Thr
915 920 925

Thr Asn Lys Tyr Ile Ala Asp Ala Leu Gly Gly Asp Ala Glu Val Asn
930 935 940

Ala Asp Gly Thr Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Glu
945 950 955 960

Tyr Asn Asn Val Gly Asp Ala Leu Asp Ala Leu Asp Asp Asn Ala Leu
965 970 975

Leu Trp Asp Glu Thr Ala Asn Gly Gly Ala Gly Ala Tyr Asn Ala Ser
980 985 990

His Asp Gly Lys Ala Ser Ile Ile Thr Asn Val Ala Asn Gly Ser Ile
995 1000 1005

Ser Glu Asp Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Asn Ala
1010 1015 1020

Thr Asn Met Met Ile Glu Gln Asn Thr Gln Ile Ile Asn Gln Leu
1025 1030 1035

Ala Gly Asn Thr Asp Ala Thr Tyr Ile Gln Glu Asn Gly Ala Gly
1040 1045 1050

Ile Asn Tyr Val Arg Thr Asn Asp Asp Gly Leu Ala Phe Asn Asp
1055 1060 1065

Ala Ser	Ala Gln Gly Val Gly	Ala Thr Ala Ile Gly	Tyr Asn Ser
1070	1075	1080	
Val Ala	Lys Gly Asp Ser Ser	Val Ala Ile Gly Gln	Gly Ser Tyr
1085	1090	1095	
Ser Asp	Val Asp Thr Gly Ile	Ala Leu Gly Ser Ser	Ser Val Ser
1100	1105	1110	
Ser Arg	Val Ile Ala Lys Gly	Ser Arg Asp Thr Ser	Ile Thr Glu
1115	1120	1125	
Asn Gly	Val Val Ile Gly Tyr	Asp Thr Thr Asp Gly	Glu Leu Leu
1130	1135	1140	
Gly Ala	Leu Ser Ile Gly Asp	Asp Gly Lys Tyr Arg	Gln Ile Ile
1145	1150	1155	
Asn Val	Ala Asp Gly Ser Glu	Ala His Asp Ala Val	Thr Val Arg
1160	1165	1170	
Gln Leu	Gln Asn Ala Ile Gly	Ala Val Ala Thr Thr	Pro Thr Lys
1175	1180	1185	
Tyr Phe	His Ala Asn Ser Thr	Glu Glu Asp Ser Leu	Ala Val Gly
1190	1195	1200	
Thr Asp	Ser Leu Ala Met Gly	Ala Lys Thr Ile Val	Asn Gly Asp
1205	1210	1215	
Lys Gly	Ile Gly Ile Gly Tyr	Gly Ala Tyr Val Asp	Ala Asn Ala
1220	1225	1230	
Leu Asn	Gly Ile Ala Ile Gly	Ser Asn Ala Gln Val	Ile His Val
1235	1240	1245	
Asn Ser	Ile Ala Ile Gly Asn	Gly Ser Thr Thr Thr	Arg Gly Ala
1250	1255	1260	
Gln Thr	Asn Tyr Thr Ala Tyr	Asn Met Asp Ala Pro	Gln Asn Ser
1265	1270	1275	

Val Gly	Glu Phe Ser	Val Gly	Ser Ala Asp Gly	Gln	Arg Gln Ile
1280		1285		1290	
Thr Asn	Val Ala Ala Gly	Ser	Ala Asp Thr Asp	Ala	Val Asn Val
1295		1300		1305	
Gly Gln	Leu Lys Val Thr	Asp	Ala Gln Val Ser	Gln	Asn Thr Gln
1310		1315		1320	
Ser Ile	Thr Asn Leu Asp	Asn	Arg Val Thr Asn	Leu	Asp Ser Arg
1325		1330		1335	
Val Thr	Asn Ile Glu Asn	Gly	Ile Gly Asp Ile	Val	Thr Thr Gly
1340		1345		1350	
Ser Thr	Lys Tyr Phe Lys	Thr	Asn Thr Asp Gly	Val	Asp Ala Ser
1355		1360		1365	
Ala Gln	Gly Lys Asp Ser	Val	Ala Ile Gly Ser	Gly	Ser Ile Ala
1370		1375		1380	
Ala Ala	Asp Asn Ser Val	Ala	Leu Gly Thr Gly	Ser	Val Ala Thr
1385		1390		1395	
Glu Glu	Asn Thr Ile Ser	Val	Gly Ser Ser Thr	Asn	Gln Arg Arg
1400		1405		1410	
Ile Thr	Asn Val Ala Ala	Gly	Lys Asn Ala Thr	Asp	Ala Val Asn
1415		1420		1425	
Val Ala	Gln Leu Lys Ser	Ser	Glu Ala Gly Gly	Val	Arg Tyr Asp
1430					